

Crambe - Jaworski BLAST P alignment 11530-1.txt
 >lcl|3831 unnamed protein product
 Length=506

Score = 979 bits (2531), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 477/515 (92%), Positives = 485/515 (94%), Gaps = 19/515 (3%)

Query	1	MTSINVKLLYHYVITNLFNLCFFPLTAIVAGKASRLTIDDLHHLYYSYLQHNVTIAPLF	60
Sbjct	1	MTSINVKLLYHYVITNLFNLCFFPLTAIVAGKAYRLTIDDLHHLYYSYLQHNVTIAPLF	60
Query	61	AFTVFGSILYIVTRPKPVYLVEYSCYLPPTQCRSSISKVMDIFYQVRKADPFRNGTCDD	120
Sbjct	61	AFTVFGS+LYI TRPKPVYLVEYSCYLPPTHCRSSISKVMDIFYQVRKADP SRNGTCDD	120
Query	121	SWLDFLRKIQERSGLGDETHGPEGLLQVPPRKTFAAAREETEQVIVGALKNFLFENTKVN	180
Sbjct	121	SWLDFLRKIQERSGLGDETHGPEGLLQVPPRKTFAAAREETEQVI+GAL+NL+NT VNP	180
Query	181	KDIGILVNSSMFNPTPSLSAMVVNTFKLRNVRSFNLGGMGCSAGVIAIDLAKDLLHVH	240
Sbjct	181	KDIGILVNSSMFNPTPSLSAMVVNTFKLRNVRSFNLGGMGCSAGVIAIDLAKDLLHVH	240
Query	241	KNTYALVVSTENITYNIYAGDNRSMMVSNCLFRVGGAAILLSNKPDRRRRSKYELVHTVR	300
Sbjct	241	KNTYALVVSTENITYNIYAGDNRSMMVSNCLFRVGGAAILLSNKP DRRRSKYELVHTVR	300
Query	301	THTGADDKSFRVCVQGGDDENGKTGVSLSKIDITEVAGRTVKKNIATLGPLILPSEKLLFF	360
Sbjct	301	THTGADDKSFRVCVQGGDDENGK GVSLSKIDIT+VAGRTVKKNIATLGPLILPSEKLLFF	360
Query	361	VTFMAKKLFKDKVKHYVP-----IDHFCIHAGGR-----LEKNLGLAPIDFKLAAVIDV	410
Sbjct	361	VTFMKKLKFDKIKHYVPDFKLAIHFCIHAGGRAVIDVLEKNLALAPID-----	411
Query	411	VEASRSTLHRFGNTSSSIWYELAYIEAKGRMKGNKVWQIALGSGFKCNSAVWVALSNV	470
Sbjct	412	VEASRSTLHRFGNTSSSIWYELAYIEAKGRMKGNKVWQIALGSGFKCNSAVWVALNNV	471
Query	471	KASTNSPWEHCIDRYPVKIDS SAKSETRAQNGRS	505
Sbjct	472	KASTNSPWEHCIDRYPVKIDS S KSETR QNGRS	506